

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	624	(glycogen adj synthase adj kinase adj "3" or gsk\$1"3" or gsk adj "3") with inhibit\$	US-PGPUB; USPAT	OR	ON	2006/07/27 08:03
L2	161	(glycogen adj synthase adj kinase adj "3" or gsk\$1"3" or gsk adj "3") and (phosphoser\$ or phosphothr\$ or phospho\$1serine or phospho\$1threonine or phospho adj (serine or threonine or thr! or ser!))	US-PGPUB; USPAT	OR	ON	2006/07/27 08:25
L3	20	(l1 or l2) and @pd>"20060305" and (@ad<"20010103" or @rlad<"20010103")	US-PGPUB; USPAT	OR	ON	2006/07/27 08:22
L4	595	(514/7,12-16,21; 530/324-329).ccls. and (phosphoser\$ or phosphothr\$ or phospho\$1serine or phospho\$1threonine or phospho adj (serine or threonine or thr! or ser!))	US-PGPUB; USPAT	OR	ON	2006/07/27 08:09
L5	9	l4 and @pd>"20060305" and (@ad<"20010103" or @rlad<"20010103")	US-PGPUB; USPAT	OR	ON	2006/07/27 08:09
L6	9	(glycogen adj synthase adj kinase adj "3" or gsk\$1"3" or gsk adj "3") and ("530"/\$.ccls. or (514/2-21).ccls.) and @pd>"20060305" and (@ad<"20010103" or @rlad<"20010103")	US-PGPUB; USPAT	OR	ON	2006/07/27 08:13
L7	353	heat adj shock adj (factor\$1"1" or factor adj "1") or hsf\$1"1" or hsf! adj "1"	US-PGPUB; USPAT	OR	ON	2006/07/27 08:15
L8	81	(l7 same (fragment or derivative or analog\$)) or (l7 and (phosphoser\$ or phosphothr\$ or phospho\$1serine or phospho\$1threonine or phospho adj (serine or threonine or thr! or ser!)))	US-PGPUB; USPAT	OR	ON	2006/07/27 08:21
L9	15	l8 and @pd>"20051107"	US-PGPUB; USPAT	OR	ON	2006/07/27 08:16
L10	218	(camp adj response adj element adj binding or creb) and (phosphoser\$ or phosphothr\$ or phospho\$1serine or phospho\$1threonine or phospho adj (serine or threonine or thr! or ser!))	US-PGPUB; USPAT	OR	ON	2006/07/27 08:21
L11	9	l10 and @pd>"20060305" and (@ad<"20010103" or @rlad<"20010103")	US-PGPUB; USPAT	OR	ON	2006/07/27 08:22

EAST Search History

L12	4	((glycogen adj synthase adj kinase adj "3" or gsk\$1"3" or gsk adj "3") and (phosphoser\$ or phosphothr\$ or phospho\$1serine or phospho\$1threonine or phospho adj (serine or threonine or thr! or ser!))). clm.	US-PGPUB; USPAT	OR	ON	2006/07/27 08:25
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Checked L3, L5, L6, L9, L11, L12
JR
7-27-2006

Interference Search History

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

JR

7.27.2006

OM protein - protein search, using sw model

Run on: July 25, 2006, 18:24:14 ; Search time 52 Seconds
(without alignments)
18.516 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents_AA:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	63	100.0	11	2	US-09-951-902-7	Sequence 7, Appli
2	60	95.2	305	2	US-10-094-749-1734	Sequence 1734, Ap
3	60	95.2	490	2	US-09-949-016-7914	Sequence 7914, Ap
4	60	95.2	529	1	US-08-178-477B-32	Sequence 32, Appli
5	60	95.2	529	2	US-09-304-121-2	Sequence 2, Appli
6	60	95.2	783	2	US-09-513-783A-176	Sequence 176, App
7	60	95.2	783	2	US-10-100-957A-176	Sequence 176, App
8	57	90.5	11	2	US-09-951-902-8	Sequence 8, Appli
9	48.5	77.0	562	2	US-10-104-047-3214	Sequence 3214, Ap
10	47	74.6	19	2	US-08-630-915A-170	Sequence 170, App

11	47	74.6	19	2	US-09-879-957-170	Sequence 170, App
12	45	71.4	559	2	US-09-716-964B-182	Sequence 182, App
13	45	71.4	564	2	US-09-248-796A-20544	Sequence 20544, A
14	44	69.8	128	2	US-09-489-039A-10886	Sequence 10886, A
15	44	69.8	285	2	US-10-104-047-3028	Sequence 3028, Ap
16	44	69.8	722	2	US-09-949-016-6909	Sequence 6909, Ap
17	44	69.8	725	2	US-09-949-016-10832	Sequence 10832, A
18	44	69.8	958	2	US-09-706-594-5	Sequence 5, Appli
19	44	69.8	966	2	US-09-964-956-32	Sequence 32, Appl
20	44	69.8	1026	2	US-09-316-048B-9	Sequence 9, Appli
21	43.5	69.0	25	1	US-08-942-423-25	Sequence 25, Appl
22	43	68.3	15	2	US-08-602-999A-373	Sequence 373, App
23	43	68.3	15	2	US-09-500-124-373	Sequence 373, App
24	43	68.3	35	2	US-09-471-276-1402	Sequence 1402, Ap
25	43	68.3	66	2	US-09-513-999C-5468	Sequence 5468, Ap
26	43	68.3	136	2	US-09-621-976-6751	Sequence 6751, Ap
27	43	68.3	147	1	US-08-756-749C-1	Sequence 1, Appli
28	43	68.3	148	2	US-09-513-999C-5869	Sequence 5869, Ap
29	43	68.3	151	2	US-09-621-976-4549	Sequence 4549, Ap
30	43	68.3	324	2	US-09-949-016-7664	Sequence 7664, Ap
31	43	68.3	505	2	US-09-949-016-6538	Sequence 6538, Ap
32	43	68.3	521	2	US-09-949-016-8809	Sequence 8809, Ap
33	43	68.3	533	2	US-09-949-016-6629	Sequence 6629, Ap
34	43	68.3	545	2	US-09-252-991A-30417	Sequence 30417, A
35	43	68.3	602	2	US-09-949-016-10221	Sequence 10221, A
36	43	68.3	750	2	US-09-949-016-11166	Sequence 11166, A
37	43	68.3	802	2	US-09-949-016-6235	Sequence 6235, Ap
38	43	68.3	984	2	US-08-764-870-15	Sequence 15, Appl
39	43	68.3	984	2	US-08-980-115-15	Sequence 15, Appl
40	43	68.3	984	2	US-09-976-594-127	Sequence 127, App
41	43	68.3	2972	2	US-09-579-181-2	Sequence 2, Appli
42	43	68.3	3118	2	US-09-579-181-1	Sequence 1, Appli
43	43	68.3	4019	2	US-09-854-133-425	Sequence 425, App
44	42	66.7	15	2	US-08-602-999A-423	Sequence 423, App
45	42	66.7	15	2	US-09-500-124-423	Sequence 423, App
46	42	66.7	102	2	US-09-902-540-10936	Sequence 10936, A
47	42	66.7	160	2	US-09-270-767-59046	Sequence 59046, A
48	42	66.7	290	2	US-09-949-016-10385	Sequence 10385, A
49	42	66.7	291	2	US-09-248-796A-20587	Sequence 20587, A
50	42	66.7	294	2	US-09-270-767-36084	Sequence 36084, A

ALIGNMENTS

RESULT 1

US-09-951-902-7

; Sequence 7, Application US/09951902

; Patent No. 6780625

; GENERAL INFORMATION:

; APPLICANT: ELDAR-FINKELMAN, Hagit

; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS

; FILE REFERENCE: ELDAR-FINK=1.1B

; CURRENT APPLICATION NUMBER: US/09/951,902

; CURRENT FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: PCT/US01/00123

; PRIOR FILING DATE: 2001-01-03

; PRIOR APPLICATION NUMBER: 60/206,115

; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Ser residue 10 is phosphorylated.
US-09-951-902-7

Query Match 100.0%; Score 63; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEEPPAPPQSP 11
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Db 1 KEEPPAPPQSP 11

RESULT 10

US-08-630-915A-170

; Sequence 170, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-170

Query Match 74.6%; Score 47; DB 2; Length 19;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EEPPAPPQSP 11
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Db 3 EEPPAPPPPP 12

Search completed: July 25, 2006, 18:25:33
Job time : 59 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 25, 2006, 18:36:20 ; Search time 187 Seconds
(without alignments)
27.248 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	63	100.0	11	3	US-09-951-902-7	Sequence 7, Appli
2	63	100.0	11	4	US-10-810-578-7	Sequence 7, Appli
3	60	95.2	13	5	US-10-862-195-1203	Sequence 1203, Ap
4	60	95.2	305	4	US-10-094-749-1734	Sequence 1734, Ap
5	60	95.2	464	5	US-10-741-600-1343	Sequence 1343, Ap
6	60	95.2	529	4	US-10-046-420-2	Sequence 2, Appli
7	60	95.2	529	5	US-10-732-923-6700	Sequence 6700, Ap
8	60	95.2	529	5	US-10-732-923-6701	Sequence 6701, Ap
9	60	95.2	529	5	US-10-756-149-5144	Sequence 5144, Ap
10	60	95.2	529	5	US-10-996-420-2	Sequence 2, Appli
11	60	95.2	529	5	US-10-984-917-2	Sequence 2, Appli

12	60	95.2	783	4	US-10-100-957A-176	Sequence 176, App
13	57	90.5	11	3	US-09-951-902-8	Sequence 8, Appli
14	57	90.5	11	4	US-10-810-578-8	Sequence 8, Appli
15	54	85.7	382	3	US-09-925-298-484	Sequence 484, App
16	54	85.7	382	4	US-10-102-806-484	Sequence 484, App
17	52	82.5	486	5	US-10-732-923-6451	Sequence 6451, Ap
18	52	82.5	503	5	US-10-732-923-6443	Sequence 6443, Ap
19	52	82.5	525	5	US-10-732-923-6441	Sequence 6441, Ap
20	50	79.4	105	4	US-10-437-963-176405	Sequence 176405,
21	49	77.8	231	4	US-10-437-963-202972	Sequence 202972,
22	48.5	77.0	562	4	US-10-104-047-3214	Sequence 3214, Ap
23	48.5	77.0	562	6	US-11-072-512-3214	Sequence 3214, Ap
24	48	76.2	126	4	US-10-425-115-220523	Sequence 220523,
25	48	76.2	172	4	US-10-425-115-343387	Sequence 343387,
26	48	76.2	230	4	US-10-424-599-191232	Sequence 191232,
27	48	76.2	491	5	US-10-732-923-6698	Sequence 6698, Ap
28	48	76.2	1024	4	US-10-437-963-139805	Sequence 139805,
29	47	74.6	19	3	US-09-879-957-170	Sequence 170, App
30	47	74.6	19	4	US-10-807-856-170	Sequence 170, App
31	47	74.6	153	4	US-10-424-599-280543	Sequence 280543,
32	47	74.6	210	6	US-11-087-099-12364	Sequence 12364, A
33	47	74.6	432	6	US-11-140-417-4	Sequence 4, Appli
34	47	74.6	473	4	US-10-437-963-202538	Sequence 202538,
35	47	74.6	537	4	US-10-437-963-188969	Sequence 188969,
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38	46	73.0	282	4	US-10-389-566-2145	Sequence 2145, Ap
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41	46	73.0	295	4	US-10-017-161-2018	Sequence 2018, Ap
42	46	73.0	295	4	US-10-292-798-1664	Sequence 1664, Ap
43	46	73.0	297	4	US-10-437-963-168840	Sequence 168840,
44	46	73.0	308	5	US-10-343-903-1	Sequence 1, Appli
45	46	73.0	388	4	US-10-437-963-152798	Sequence 152798,
46	46	73.0	447	4	US-10-072-012-24	Sequence 24, Appl
47	46	73.0	472	4	US-10-072-012-30	Sequence 30, Appl
48	46	73.0	724	4	US-10-416-898-18	Sequence 18, Appl
49	45	71.4	104	4	US-10-425-115-313062	Sequence 313062,
50	45	71.4	110	4	US-10-424-599-191233	Sequence 191233,

ALIGNMENTS

RESULT 1

US-09-951-902-7

; Sequence 7, Application US/09951902

; Patent No. US20020147146A1

; GENERAL INFORMATION:

; APPLICANT: ELDAR-FINKELMAN, Hagit

; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS

; FILE REFERENCE: ELDAR-FINK=1.1B

; CURRENT APPLICATION NUMBER: US/09/951,902

; CURRENT FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: PCT/US01/00123

; PRIOR FILING DATE: 2001-01-03

; PRIOR APPLICATION NUMBER: 60/206,115

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: 60/174,308
; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Ser residue 10 is phosphorylated.
US-09-951-902-7

Query Match 100.0%; Score 63; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEEPPAPPQSP 11
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Db 1 KEEPPAPPQSP 11

RESULT 2

US-10-810-578-7
; Sequence 7, Application US/10810578
; Publication No. US20040162234A1
; GENERAL INFORMATION:
; APPLICANT: ELDAR-FINKELMAN, Hagit
; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
; FILE REFERENCE: 27457
; CURRENT APPLICATION NUMBER: US/10/810,578
; CURRENT FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Ser residue 10 is phosphorylated.
US-10-810-578-7

Query Match 100.0%; Score 63; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEEPPAPPQSP 11
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Db 1 KEEPPAPPQSP 11

Search completed: July 25, 2006, 18:39:49
Job time : 202 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 25, 2006, 18:36:40 ; Search time 29 Seconds
(without alignments)
21.874 Million cell updates/sec

Title: US-10-810-578-7
Perfect score: 63
Sequence: 1 KEEPPAPPQSP 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	63	100.0	11	6	US-10-538-171-8	Sequence 8, Appli
2	63	100.0	11	6	US-10-538-171-10	Sequence 10, Appl
3	60	95.2	11	6	US-10-538-171-7	Sequence 7, Appli
4	59	93.7	11	6	US-10-538-171-11	Sequence 11, Appl
5	57	90.5	11	6	US-10-538-171-9	Sequence 9, Appli
6	57	90.5	12	6	US-10-538-171-16	Sequence 16, Appl
7	57	90.5	12	6	US-10-538-171-18	Sequence 18, Appl
8	50	79.4	13	6	US-10-538-171-17	Sequence 17, Appl
9	47	74.6	108	6	US-10-449-902-42364	Sequence 42364, A

10	47	74.6	108	6	US-10-449-902-49671	Sequence 49671, A
11	47	74.6	108	6	US-10-449-902-53083	Sequence 53083, A
12	45	71.4	445	6	US-10-953-349-39517	Sequence 39517, A
13	45	71.4	490	6	US-10-953-349-39516	Sequence 39516, A
14	45	71.4	520	6	US-10-953-349-39515	Sequence 39515, A
15	45	71.4	656	7	US-11-056-355B-89084	Sequence 89084, A
16	45	71.4	656	7	US-11-056-355B-92840	Sequence 92840, A
17	45	71.4	670	7	US-11-056-355B-107649	Sequence 107649,
18	45	71.4	670	7	US-11-056-355B-118888	Sequence 118888,
19	45	71.4	674	7	US-11-056-355B-69475	Sequence 69475, A
20	45	71.4	681	6	US-10-953-349-10919	Sequence 10919, A
21	45	71.4	681	7	US-11-056-355B-45477	Sequence 45477, A
22	45	71.4	681	7	US-11-056-355B-49007	Sequence 49007, A
23	44	69.8	583	6	US-10-449-902-56584	Sequence 56584, A
24	43	68.3	139	6	US-10-953-349-27191	Sequence 27191, A
25	43	68.3	167	6	US-10-449-902-33946	Sequence 33946, A
26	43	68.3	301	7	US-11-056-355B-65949	Sequence 65949, A
27	43	68.3	316	7	US-11-056-355B-65948	Sequence 65948, A
28	43	68.3	827	6	US-10-449-902-56545	Sequence 56545, A
29	43	68.3	984	7	US-11-283-329-104	Sequence 104, App
30	43	68.3	3475	7	US-11-063-439-67	Sequence 67, Appl
31	43	68.3	3494	7	US-11-063-439-50	Sequence 50, Appl
32	43	68.3	3503	7	US-11-063-439-23	Sequence 23, Appl
33	43	68.3	3507	7	US-11-063-439-70	Sequence 70, Appl
34	43	68.3	3519	7	US-11-063-439-92	Sequence 92, Appl
35	43	68.3	3593	7	US-11-063-439-20	Sequence 20, Appl
36	43	68.3	3651	7	US-11-063-439-268	Sequence 268, App
37	43	68.3	3661	7	US-11-063-439-281	Sequence 281, App
38	42	66.7	97	7	US-11-056-355B-62248	Sequence 62248, A
39	42	66.7	176	7	US-11-056-355B-62245	Sequence 62245, A
40	42	66.7	210	6	US-10-449-902-50498	Sequence 50498, A
41	42	66.7	266	6	US-10-449-902-48647	Sequence 48647, A
42	42	66.7	286	6	US-10-449-902-37751	Sequence 37751, A
43	42	66.7	371	6	US-10-449-902-49630	Sequence 49630, A
44	42	66.7	409	6	US-10-953-349-27801	Sequence 27801, A
45	42	66.7	409	7	US-11-056-355B-64803	Sequence 64803, A
46	42	66.7	428	6	US-10-449-902-44039	Sequence 44039, A
47	42	66.7	490	6	US-10-449-902-56644	Sequence 56644, A
48	42	66.7	491	6	US-10-449-902-37403	Sequence 37403, A
49	42	66.7	659	7	US-11-105-233-48	Sequence 48, Appl
50	42	66.7	770	6	US-10-449-902-53211	Sequence 53211, A

ALIGNMENTS

RESULT 1
 US-10-538-171-8
 ; Sequence 8, Application US/10538171
 ; Publication No. US20060135408A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eldar-Finkelman, Hagit
 ; TITLE OF INVENTION: GLYCOGEN SYNTHASE KINASE-3 INHIBITORS
 ; FILE REFERENCE: 29724
 ; CURRENT APPLICATION NUMBER: US/10/538,171
 ; CURRENT FILING DATE: 2005-06-09

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: PHOSPHORYLATION
US-10-538-171-8

Query Match 100.0%; Score 63; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KEEPPAPPQSP 11

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Job time : 38 secs